

SEQUENCE LISTING

<110> Garcia-Martinez, Leon Fernando
Chen, Yuching
Andrews, Dawn
Celltech R&D, Inc.

<120> Modulating Immune Responses

<130> 1427.008US1

<160> 99

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2051

<212> DNA

<213> Mus musculus

<400> 1

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<210> 2

<211> 196

<212> PRT

<213> Mus musculus

<400> 2

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Pro	Val	Thr	Ser	Pro	Ser	Lys	His	Leu	Gly	Pro	Val	Thr	Leu	Pro	Lys
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Thr	Glu	Thr	Val												
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<210> 3

<211> 2051

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic mutant CD83 sequence

<400> 3

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tcaaagaaga	atttttcatg	ttttttcaaa	gaagtgtgtt	tctttccttt	tttaaaatat	1320
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<210> 4
 <211> 251
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A synthetic mutant CD83 sequence

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<400> 4
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          20          25          30
Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
          35          40          45
Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
          50          55          60
Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala
65          70          75          80
Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
          85          90          95
Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
          100          105          110
Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
          115          120          125
Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
          130          135          140
Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
145          150          155          160
Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
          165          170          175

Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys
          180          185          190
Thr Glu Thr Val Arg Val Gly Ser Pro Leu Val Phe Thr Lys Pro Arg
          195          200          205
Ala His Gln Ile Ser Val Pro Glu Cys His Pro Asp Lys Arg Arg Met
          210          215          220
Ser Ser Ile Leu Arg Trp Gln Pro Phe Phe Glu Val Leu His Leu Thr
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Val Gly Ser Thr Leu Leu Pro Asp Thr Gly Ser
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<210> 5
 <211> 756
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A synthetic mutant CD83 sequence

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<400> 5
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tattccctga cgatccaaaa cactaccatc tgcagctcgg gcacctacag gtgtgccctg      300
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<210> 6

<400> 6
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<210> 7

<211> 168

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic mutant CD83 sequence

<400> 7

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<210> 8

<211> 55

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic mutant CD83 sequence

<400> 8

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Arg Val Gly Ser Pro Leu Val Phe Thr Lys Pro Arg Ala His Gln Ile
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Ser Val Pro Glu Cys His Pro Asp Lys Arg Arg Met Ser Ser Ile Leu
          20          25          30
Arg Trp Gln Pro Phe Phe Glu Val Leu His Leu Thr Val Gly Ser Thr
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Leu Leu Pro Asp Thr Gly Ser
          50          55

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<210> 9

<211> 205

<212> PRT

<213> Homo sapiens

<400> 9

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Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
          20          25          30

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Trp	Val	Lys	Leu	Leu	Glu	Gly	Gly	Glu	Glu	Arg	Met	Glu	Thr	Pro	Gln
	50					55					60				
Glu	Asp	His	Leu	Arg	Gly	Gln	His	Tyr	His	Gln	Lys	Gly	Gln	Asn	Gly
65					70					75				80	
Ser	Phe	Asp	Ala	Pro	Asn	Glu	Arg	Pro	Tyr	Ser	Leu	Lys	Ile	Arg	Asn
			85					90						95	
Thr	Thr	Ser	Cys	Asn	Ser	Gly	Thr	Tyr	Arg	Cys	Thr	Leu	Gln	Asp	Pro
			100					105					110		
Asp	Gly	Gln	Arg	Asn	Leu	Ser	Gly	Lys	Val	Ile	Leu	Arg	Val	Thr	Gly
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Cys	Pro	Ala	Gln	Arg	Lys	Glu	Glu	Thr	Phe	Lys	Lys	Tyr	Arg	Ala	Glu
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Ile	Val	Leu	Leu	Leu	Ala	Leu	Val	Ile	Phe	Tyr	Leu	Thr	Leu	Ile	Ile
145					150					155					160
Phe	Thr	Cys	Lys	Phe	Ala	Arg	Leu	Gln	Ser	Ile	Phe	Pro	Asp	Phe	Ser
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Lys	Ala	Gly	Met	Glu	Arg	Ala	Phe	Leu	Pro	Val	Thr	Ser	Pro	Asn	Lys
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	195						200					205			

<210> 10
 <211> 2574
 <212> DNA
 <213> Homo sapiens

<400> 10

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<210> 11

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic 20D04 light chain sequence

<400> 11

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          20           25           30
Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ala
          35           40           45
Ser Glu Ser Ile Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
 50           55           60
Gln Pro Pro Lys Leu Leu Ile Tyr Arg Thr Ser Thr Leu Ala Ser Gly
65           70           75           80
Val Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu
          85           90           95
Thr Ile Ser Gly Val Gln Cys Asp Asp Val Ala Thr Tyr Tyr Cys Gln
          100          105          110
Cys Thr Ser Gly Gly Lys Phe Ile Ser Asp Gly Ala Ala Phe Gly Gly
          115          120          125
Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu
          130          135          140
Leu Phe Pro Pro Ser Ser Asp Glu Val Ala Thr Gly Thr Val Thr Ile
145          150          155          160
Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu
          165          170          175
Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro
          180          185          190
Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
          195          200          205
Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr
          210          215          220
Gln Gly Thr Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys
225          230          235

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<210> 12

<211> 720

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic 20D04 anti-CD83 light chain sequence

<400> 12

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acagtcacca	tcaattgcc	ggccagtgaa	agcattagca	actacttata	ctggtatcag	180
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gtctcatcgc	ggttcaaagg	cagtggatct	gggacagagt	acactctcac	catcagcggc	300
gtgcagtgtg	acgatgttgc	cacttactac	tgtcaatgca	cttctggtgg	gaagttcatt	360
agtgatggg	ctgcttttcg	cggagggacc	gaggtggtgg	tcaaagggtga	tccagttgca	420
cctactgtcc	tcctcttccc	accatctagc	gatgaggtgg	caactggaac	agtcaccatc	480
gtgtgtgtgg	cgaataaata	ctttcccgat	gtcaccgtca	cctgggaggt	ggatggcacc	540
acccaaacaa	ctggcatcga	gaacagtaaa	acaccgcaga	attctgcaga	ttgtacctac	600
aacctcagca	gcactctgac	actgaccagc	acacagtaca	acagccacaa	agagtacacc	660
tgcaagggtga	cccagggcac	gacctcagtc	gtccagagct	tcagtaggaa	gaactgttaa	720

<210> 13

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic 20D04 heavy chain sequence

<400> 13

Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly
1				5				10					15		
Val	Gln	Cys	Gln	Ser	Val	Glu	Glu	Ser	Gly	Gly	Arg	Leu	Val	Thr	Pro
			20					25				30			
Gly	Thr	Pro	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Ser
			35				40				45				
Asn	Asn	Ala	Ile	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu
	50				55			60							
Trp	Ile	Gly	Tyr	Ile	Trp	Ser	Gly	Gly	Leu	Thr	Tyr	Tyr	Ala	Asn	Trp
65				70				75						80	
Ala	Glu	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Thr	Ser	Thr	Thr	Val	Asp	Leu
			85					90					95		
Lys	Met	Thr	Ser	Pro	Thr	Ile	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	Ala
			100					105					110		
Arg	Gly	Ile	Asn	Asn	Ser	Ala	Leu	Trp	Gly	Pro	Gly	Thr	Leu	Val	Thr
		115				120					125				
Val	Ser	Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro
		130				135					140				
Cys	Cys	Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	Thr	Leu	Gly	Cys	Leu	Val
145				150				155						160	
Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Thr
			165					170						175	
Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val	Arg	Gln	Ser	Ser	Gly
		180					185					190			
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr	Ser	Ser	Ser	Gln	Pro
		195				200					205				
Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn	Thr	Lys	Val	Asp	Lys
		210				215					220				
Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr	Cys	Pro	Pro	Pro	Glu
225				230						235					240
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp
			245					250						255	
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
		260						265					270		
Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr	Trp	Tyr	Ile	Asn	Asn
		275				280					285				
Glu	Gln	Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg	Glu	Gln	Gln	Phe	Asn
		290				295					300				
Ser	Thr	Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile	Ala	His	Gln	Asp	Trp
305				310						315				320	
Leu	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His	Asn	Lys	Ala	Leu	Pro
			325					330						335	

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu
340 345 350
Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg
355 360 365
Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile
370 375 380
Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr
385 390 395 400
Thr Pro Ala Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Asn Lys
405 410 415
Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys
420 425 430
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile
435 440 445
Ser Arg Ser Pro Gly Lys
450

<210> 14
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic 20D04 anti-CD83 heavy chain sequence

<400> 14
atggagacag gcttgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60
tcggtggagg agtccggggg tcgcctgggc acgcctggga caccctgac actcacctgc 120
accgtctctg gattctccct cagtaacaat gcaataaact gggtcggcca ggctccaggg 180
aaggggctag agtggatcgg atacatttgg agtgggtggc ttacatacta cgcgaactgg 240
gcggaaggcc gattcaccat ctccaaaacc tcgactacgg tggatctgaa gatgaccagt 300
ccgacaatcg aggacacggc cacctatttc tgtgccagag ggattaataa ctccgctttg 360
tggggcccag gcaccctggg caccgtctcc tcaggggcaac ctaaggctcc atcagtcttc 420
ccactggccc cctgctgcgg ggacacaccc tctagcacgg tgacctggg ctgcctgggc 480
aaaggctacc tcccggagcc agtgaccgtg acctggaact cgggcaccct caccaatggg 540
gtacgcacct tcccgctcgt ccggcagtc tccaggcctc actcgtgag cagcgtgggtg 600
agcgtgacct caagcagcca gcccgtcacc tgcaacgtgg cccaccagc caccaacacc 660
aaagtggaca agaccgttgc gccctcgaca tgcagcaagc ccacgtgcc acccctgaa 720
ctcctggggg gaccgtctgt cttcatcttc ccccaaaac ccaaggacac cctcatgatc 780
tcacgcaccc ccgaggtcac atgcgtgggt gtggacgtga gccaggatga ccccgaggtg 840
cagttcacat ggtacataaa caacgagcag gtgcgcaccg cccggccgcc gctacgggag 900
cagcagttca acagcacgat ccgcgtgggc agcaccctcc ccacgcgca ccaggactgg 960
ctgaggggca aggagttcaa gtgcaaagtc cacaacaagg cactcccggc ccccatcgag 1020
aaaaccatct ccaaagccag agggcagccc ctggagccga aggtctacac catgggcccct 1080
ccccgggagg agctgagcag caggctcggtc agcctgacct gcatgatcaa cggcttctac 1140
ccttccgaca tctcgggtga gtgggagaag aacgggaagg cagaggacaa ctacaagacc 1200
acgccggccg tgctggacag cgacggctcc tacttctct acaacaagct ctcagtgcgc 1260
acgagtgaat ggcagcgggg cgacgtcttc acctgctccg tgatgcacga ggccttgac 1320
aaccactaca cgcagaagtc catctccgcg tctccgggta aa 1362

<210> 15
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic 11G05 light chain sequence

<400> 15
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp
1 5 10 15


```

Leu Pro Gly Ala Arg Cys Ala Asp Val Val Met Thr Gln Thr Pro Ala
      20      25      30
Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser
      35      40      45
Ser Lys Asn Val Tyr Asn Asn Asn Trp Leu Ser Trp Phe Gln Gln Lys
      50      55      60
Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala
      65      70      75      80
Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly Ser Gly Thr Gln Phe
      85      90      95
Thr Leu Thr Ile Ser Asp Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr
      100      105      110
Cys Ala Gly Asp Tyr Ser Ser Ser Ser Asp Asn Gly Phe Gly Gly Gly
      115      120      125
Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu
      130      135      140
Phe Pro Pro Ser Ser Asp Glu Val Ala Thr Gly Thr Val Thr Ile Val
      145      150      155      160
Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val
      165      170      175
Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln
      180      185      190
Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr
      195      200      205
Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln
      210      215      220
Gly Thr Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys
      225      230      235

```

<210> 16

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic 11G05 anti-CD83 light chain sequence

<400> 16

```

atggacacca gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc      60
agatgtgccg acgtcgtgat gaccagact ccagcctccg tgtctgcagc tgtgggaggc      120
acagtcacca tcaattgccg gtccagtaag aatgtttata ataacaactg gttatcctgg      180
tttcagcaga aaccagggca gcctcccaag ctctgatctc attatgcac cactctggca      240
tctgggggtc catcgcggtt cagaggcagt ggatctggga cacagttcac tctcaccatt      300
agcgacgtgc agtgtgacga tgctgccact tactactgtg caggcgatta tagtagtagt      360
agtgataatg gtttcggcgg agggaccgag gtggtgggtc aaggtgatcc agttgcacct      420
actgtcctcc tcttcccacc atctagcgat gaggtggcaa ctggaacagt caccatcgtg      480
tgtgtggcga ataaatactt tcccgatgtc accgtcacct gggaggtgga tggcaccacc      540
caaacaactg gcatcgagaa cagtaaaaca ccgcagaatt ctgcagattg tacctacaac      600
ctcagcagca ctctgacact gaccagcaca cagtacaaca gccacaaaga gtacacctgc      660
aaggtgaccc agggcacgac ctcagtcgtc cagagcttca gtaggaagaa ctgttaa      717

```

<210> 17

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic 11G05 heavy chain sequence

<400> 17

```

Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
  1              5              10              15

```

Val	Gln	Cys	Gln	Ser	Val	Glu	Glu	Ser	Gly	Gly	Arg	Leu	Val	Thr	Pro
			20					25					30		
Gly	Thr	Pro	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Thr	Ile	Ser
		35					40					45			
Asp	Tyr	Asp	Leu	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Glu	Gly	Leu	Lys
	50					55					60				
Tyr	Ile	Gly	Phe	Ile	Ala	Ile	Asp	Gly	Asn	Pro	Tyr	Tyr	Ala	Thr	Trp
65					70					75					80
Ala	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Thr	Ser	Thr	Thr	Val	Asp	Leu
				85					90					95	
Lys	Ile	Thr	Ala	Pro	Thr	Thr	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	Ala
			100					105						110	
Arg	Gly	Ala	Gly	Asp	Leu	Trp	Gly	Pro	Gly	Thr	Leu	Val	Thr	Val	Ser
		115					120					125			
Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Cys
	130					135					140				
Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly
145					150					155					160
Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Thr	Leu	Thr
			165						170					175	
Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val	Arg	Gln	Ser	Ser	Gly	Leu	Tyr
			180					185					190		
Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr	Ser	Ser	Ser	Gln	Pro	Val	Thr
		195					200					205			
Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn	Thr	Lys	Val	Asp	Lys	Thr	Val
	210					215					220				
Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr	Cys	Pro	Pro	Pro	Glu	Leu	Leu
225					230					235					240
Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
			245						250					255	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
			260					265					270		
Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr	Trp	Tyr	Ile	Asn	Asn	Glu	Gln
	275						280					285			
Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg	Glu	Gln	Gln	Phe	Asn	Ser	Thr
	290					295					300				
Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile	Ala	His	Gln	Asp	Trp	Leu	Arg
305					310					315					320
Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His	Asn	Lys	Ala	Leu	Pro	Ala	Pro
				325					330					335	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Arg	Gly	Gln	Pro	Leu	Glu	Pro	Lys
			340					345					350		
Val	Tyr	Thr	Met	Gly	Pro	Pro	Arg	Glu	Glu	Leu	Ser	Ser	Arg	Ser	Val
	355						360					365			
Ser	Leu	Thr	Cys	Met	Ile	Asn	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ser	Val
	370					375					380				
Glu	Trp	Glu	Lys	Asn	Gly	Lys	Ala	Glu	Asp	Asn	Tyr	Lys	Thr	Thr	Pro
385					390					395					400
Ala	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Leu	Tyr	Asn	Lys	Leu	Ser
				405					410					415	
Val	Pro	Thr	Ser	Glu	Trp	Gln	Arg	Gly	Asp	Val	Phe	Thr	Cys	Ser	Val
			420					425					430		
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Ile	Ser	Arg
	435					440						445			
Ser	Pro	Gly	Lys												
	450														

<210> 18
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>

<223> A synthetic 11G05 anti-CD83 heavy chain sequence

<400> 18

```
atggagacag gcctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag      60
tcgggtggagg agtccggggg tcgcctgggc acgcctggga cacccttgac actcacctgc     120
acagtctctg gattcaccat cagtgactac gacttgagct gggtcgcgca ggctccaggg     180
gaggggctga aatacatcgg attcattgct attgatggta acccatacta cgcgacctgg     240
gcaaaaggcc gattcaccat ctccaaaacc tcgaccacgg tggatctgaa aatcaccgct     300
ccgacaaccg aagacacggc cacgtatttc tgtgccagag gggcagggga cctctggggc     360
ccagggaccc tcgtcaccgt ctcttcaggg caacctaaagg ctccatcagt cttcccactg     420
gccccctgct gcggggacac accctctagc acggtgacct tgggctgcct ggtcaaaggc     480
tacctcccg agccagtgc cgtgacctgg aactcgggca ccctcaccaa tggggtacgc     540
accttcccgt ccgtccggca gtcctcaggc ctctactcgc tgagcagcgt ggtgagcgtg     600
acctcaagca gccagcccgt cacctgcaac gtggcccacc cagccacca caccaaagtg     660
gacaagaccg ttgcgccctc gacatgcagc aagcccacgt gccaccccc tgaactcctg     720
gggggaccgt ctgtcttcat cttcccccca aaacccaagg acaccctcat gatctcacgc     780
acccccgagg tcacatgcgt ggtggtggac gtgagccagg atgacccccg ggtgcagttc     840
acatggtaca taaacaacga gcaggtgcgc accgcccggc cgcgctacg ggagcagcag     900
ttcaacagca cgatccgcgt ggtcagcacc ctccccatcg cgcaccagga ctgggtgagg     960
ggcaaggagt tcaagtgcaa agtcacaac aaggcactcc cggcccccat cgagaaaacc    1020
atctccaaag ccagagggca gcccctggag ccgaaggctt acaccatggg ccctccccgg    1080
gaggagctga gcagcaggtc ggtcagcctg acctgcata tcaacggctt ctacccttcc    1140
gacatctcgg tggagtggga gaagaacggg aaggcagagg acaactaaa gaccacgccg    1200
gccgtgctgg acagcgacgg ctctacttcc ctctacaaca agctctcagt gccacgagt    1260
gagtggcagc ggggcgacgt cttcacctgc tccgtgatgc acgaggcctt gcacaaccac    1320
tacacgcaga agtccatctc ccgctctccg ggtaaa                                1356
```

<210> 19

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<221> SITE

<222> (1)...(238)

<223> Xaa = any amino acid

<220>

<223> A synthetic 14C12 light chain sequence

<400> 19

```
Met Asp Xaa Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1          5          10          15
Leu Pro Gly Ala Arg Cys Ala Leu Val Met Thr Gln Thr Pro Ala Ser
 20          25          30
Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser Ser
 35          40          45
Gln Ser Val Tyr Asp Asn Asp Glu Leu Ser Trp Tyr Gln Gln Lys Pro
 50          55          60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Lys Leu Ala Ser
 65          70          75          80
Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Ala
 85          90          95
Leu Thr Ile Ser Gly Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys
100          105          110
Gln Ala Thr His Tyr Ser Ser Asp Trp Tyr Leu Thr Phe Gly Gly Gly
115          120          125
Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu
130          135          140
Phe Pro Pro Ser Ser Asp Glu Val Ala Thr Gly Thr Val Thr Ile Val
145          150          155          160
```

Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val
165 170 175
Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln
180 185 190
Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr
195 200 205
Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln
210 215 220
Gly Thr Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys
225 230 235

<210> 20
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic 14C12 anti-CD83 light chain sequence

<400> 20
atggacatra gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60
agatgtgccc ttgtgatgac ccagactcca gcctccgtgt ctgcagctgt gggaggcaca 120
gtcaccatca attgccagtc cagtcagagt gtttatgata acgacgaatt atcctggtat 180
cagcagaaac cagggcagcc tcccaagctc ctgatctatc tggcatccaa gttggcatct 240
ggggtcccat cccgattcaa aggcagtgga tctgggacac agttcgctct caccatcagc 300
ggcgtgcagt gtgacgatgc tgccacttac tactgtcaag ccactcatta tagtagtgat 360
tggtatctta ctttcggcgg agggaccgag gtggtggtca aaggtgatcc agttgcacct 420
actgtcctcc tcttcccacc atctagcgat gaggtggcaa ctggaacagt caccatcgtg 480
tgtgtggcga ataaatactt tcccgatgtc accgtcacct gggaggtgga tggcaccacc 540
caaacaactg gcctcgagaa cagtaaaaca ccgcagaatt ctgcagattg tacctacaac 600
ctcagcagca ctctgacact gaccagcaca cagtacaaca gccacaaaga gtacacctgc 660
aaggtgaccc agggcacgac ctcagtcgtc cagagcttca gtaggaagaa ctgttaa 717

<210> 21
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic 14C12 heavy chain sequence

<400> 21
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15
Val His Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
20 25 30
Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Arg Ser
35 40 45
Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60
Trp Val Gly Val Ile Ser Thr Ala Tyr Asn Ser His Tyr Ala Ser Trp
65 70 75 80
Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu
85 90 95
Lys Met Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
100 105 110
Arg Gly Gly Ser Trp Leu Asp Leu Trp Gly Gln Gly Thr Leu Val Thr
115 120 125
Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro
130 135 140
Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys Leu Val
145 150 155 160

Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Thr
				165					170					175	
Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val	Arg	Gln	Ser	Ser	Gly
			180					185					190		
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr	Ser	Ser	Ser	Gln	Pro
		195					200					205			
Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn	Thr	Lys	Val	Asp	Lys
	210					215				220					
Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr	Cys	Pro	Pro	Pro	Glu
225					230					235					240
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp
				245					250					255	
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
			260					265					270		
Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr	Trp	Tyr	Ile	Asn	Asn
	275						280					285			
Glu	Gln	Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg	Glu	Gln	Gln	Phe	Asn
	290					295				300					
Ser	Thr	Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile	Ala	His	Gln	Asp	Trp
305					310					315					320
Leu	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His	Asn	Lys	Ala	Leu	Pro
				325					330					335	
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Arg	Gly	Gln	Pro	Leu	Glu
			340					345					350		
Pro	Lys	Val	Tyr	Thr	Met	Gly	Pro	Pro	Arg	Glu	Glu	Leu	Ser	Ser	Arg
	355						360					365			
Ser	Val	Ser	Leu	Thr	Cys	Met	Ile	Asn	Gly	Phe	Tyr	Pro	Ser	Asp	Ile
	370					375					380				
Ser	Val	Glu	Trp	Glu	Lys	Asn	Gly	Lys	Ala	Glu	Asp	Asn	Tyr	Lys	Thr
385					390					395					400
Thr	Pro	Ala	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Leu	Tyr	Asn	Lys
				405					410					415	
Leu	Ser	Val	Pro	Thr	Ser	Glu	Trp	Gln	Arg	Gly	Asp	Val	Phe	Thr	Cys
			420					425					430		
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Ile
	435						440					445			
Ser	Arg	Ser	Pro	Gly	Lys										
	450														

<210> 22

<211> 1362

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic 14C12 anti-CD83 heavy chain sequence

<400> 22

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Gly	Cys	Thr	Gly	Gly	Cys	Thr	Thr	Cys	Thr	Cys	Cys	Thr	Gly	Gly	Thr
			20					25					30		
Cys	Gly	Cys	Thr	Gly	Thr	Gly	Cys	Thr	Cys	Ala	Ala	Ala	Gly	Gly	Thr
		35					40					45			
Gly	Thr	Cys	Cys	Ala	Cys	Thr	Gly	Thr	Cys	Ala	Gly	Thr	Cys	Gly	Gly
	50					55					60				
Thr	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Thr	Cys	Cys	Gly	Gly	Gly	Gly	Gly
65					70					75					80
Thr	Cys	Gly	Cys	Cys	Thr	Gly	Gly	Thr	Cys	Ala	Cys	Gly	Cys	Cys	Thr
				85					90					95	
Gly	Gly	Gly	Ala	Cys	Ala	Cys	Cys	Cys	Cys	Thr	Gly	Ala	Cys	Ala	Cys
			100					105						110	

Thr	Cys	Ala	Cys	Cys	Thr	Gly	Cys	Ala	Cys	Ala	Gly	Cys	Cys	Thr	Cys	
		115					120					125				
Thr	Gly	Gly	Ala	Thr	Thr	Cys	Thr	Cys	Cys	Cys	Gly	Cys	Ala	Gly	Cys	
	130					135					140					
Ala	Gly	Cys	Thr	Ala	Cys	Gly	Ala	Cys	Ala	Thr	Gly	Ala	Gly	Cys	Thr	
145					150					155					160	
Gly	Gly	Gly	Thr	Cys	Cys	Gly	Cys	Cys	Ala	Gly	Gly	Cys	Thr	Cys	Cys	
			165						170					175		
Ala	Gly	Gly	Gly	Ala	Ala	Gly	Gly	Gly	Gly	Cys	Thr	Gly	Gly	Ala	Ala	
		180						185					190			
Thr	Gly	Gly	Gly	Thr	Cys	Gly	Gly	Ala	Gly	Thr	Cys	Ala	Thr	Thr	Ala	
	195						200					205				
Gly	Thr	Ala	Cys	Thr	Gly	Cys	Thr	Thr	Ala	Thr	Ala	Ala	Cys	Thr	Cys	
	210					215					220					
Ala	Cys	Ala	Cys	Thr	Ala	Cys	Gly	Cys	Gly	Ala	Gly	Cys	Thr	Gly	Gly	
225					230					235					240	
Gly	Cys	Ala	Ala	Ala	Ala	Gly	Gly	Cys	Cys	Gly	Ala	Thr	Thr	Cys	Ala	
			245						250					255		
Cys	Cys	Ala	Thr	Cys	Thr	Cys	Cys	Ala	Gly	Ala	Ala	Cys	Cys	Thr	Cys	
		260						265					270			
Gly	Ala	Cys	Cys	Ala	Cys	Gly	Gly	Thr	Gly	Gly	Ala	Thr	Cys	Thr	Gly	
	275						280					285				
Ala	Ala	Ala	Ala	Thr	Gly	Ala	Cys	Cys	Ala	Gly	Thr	Cys	Thr	Gly	Ala	
	290					295				300						
Cys	Ala	Ala	Cys	Cys	Gly	Ala	Ala	Gly	Ala	Cys	Ala	Cys	Gly	Gly	Cys	
305					310					315					320	
Cys	Ala	Cys	Cys	Thr	Ala	Thr	Thr	Thr	Cys	Thr	Gly	Thr	Gly	Cys	Cys	
			325						330					335		
Ala	Gly	Ala	Gly	Gly	Gly	Gly	Gly	Thr	Ala	Gly	Thr	Thr	Gly	Gly	Thr	
		340						345					350			
Thr	Gly	Gly	Ala	Thr	Cys	Thr	Cys	Thr	Gly	Gly	Gly	Gly	Cys	Cys	Ala	
	355						360					365				
Gly	Gly	Gly	Cys	Ala	Cys	Cys	Cys	Thr	Gly	Gly	Thr	Cys	Ala	Cys	Cys	
	370					375					380					
Gly	Thr	Cys	Thr	Cys	Cys	Thr	Cys	Ala	Gly	Gly	Gly	Cys	Ala	Ala	Cys	
385					390					395					400	
Cys	Thr	Ala	Ala	Gly	Gly	Cys	Thr	Cys	Cys	Ala	Thr	Cys	Ala	Gly	Thr	
			405						410					415		
Cys	Thr	Thr	Cys	Cys	Cys	Ala	Cys	Thr	Gly	Gly	Cys	Cys	Cys	Cys	Cys	
		420						425					430			
Thr	Gly	Cys	Thr	Gly	Cys	Gly	Gly	Gly	Gly	Ala	Cys	Ala	Cys	Ala	Cys	
	435						440					445				
Cys	Cys	Thr	Cys	Thr	Ala	Gly	Cys	Ala	Cys	Gly	Gly	Thr	Gly	Ala	Cys	
	450					455					460					
Cys	Thr	Thr	Gly	Gly	Gly	Cys	Thr	Gly	Cys	Cys	Thr	Gly	Gly	Thr	Cys	
465					470					475					480	
Ala	Ala	Ala	Gly	Gly	Cys	Thr	Ala	Cys	Cys	Thr	Cys	Cys	Cys	Gly	Gly	
			485						490					495		
Ala	Gly	Cys	Cys	Ala	Gly	Thr	Gly	Ala	Cys	Cys	Gly	Thr	Gly	Ala	Cys	
		500						505					510			
Cys	Thr	Gly	Gly	Ala	Ala	Cys	Thr	Cys	Gly	Gly	Gly	Cys	Ala	Cys	Cys	
	515							520				525				
Cys	Thr	Cys	Ala	Cys	Cys	Ala	Ala	Thr	Gly	Gly	Gly	Gly	Thr	Ala	Cys	
	530					535					540					
Gly	Cys	Ala	Cys	Cys	Thr	Thr	Cys	Cys	Cys	Gly	Thr	Cys	Cys	Gly	Thr	
545					550					555					560	
Cys	Cys	Gly	Gly	Cys	Ala	Gly	Thr	Cys	Cys	Thr	Cys	Ala	Gly	Gly	Cys	
			565						570					575		
Cys	Thr	Cys	Thr	Ala	Cys	Thr	Cys	Gly	Cys	Thr	Gly	Ala	Gly	Cys	Ala	
		580						585					590			
Gly	Cys	Gly	Thr	Gly	Gly	Thr	Gly	Ala	Gly	Cys	Gly	Thr	Gly	Ala	Cys	
	595						600					605				

Cys	Thr	Cys	Ala	Ala	Gly	Cys	Ala	Gly	Cys	Cys	Ala	Gly	Cys	Cys	Cys			
	610						615				620							
Gly	Thr	Cys	Ala	Cys	Cys	Thr	Gly	Cys	Ala	Ala	Cys	Gly	Thr	Gly	Gly			
	625						630				635							640
Cys	Cys	Cys	Ala	Cys	Cys	Cys	Ala	Gly	Cys	Cys	Ala	Cys	Cys	Ala	Ala			
				645						650					655			
Cys	Ala	Cys	Cys	Ala	Ala	Ala	Gly	Thr	Gly	Gly	Ala	Cys	Ala	Ala	Gly			
			660					665					670					
Ala	Cys	Cys	Gly	Thr	Thr	Gly	Cys	Gly	Cys	Cys	Cys	Thr	Cys	Gly	Ala			
	675						680					685						
Cys	Ala	Thr	Gly	Cys	Ala	Gly	Cys	Ala	Ala	Gly	Cys	Cys	Cys	Ala	Cys			
	690						695				700							
Gly	Thr	Gly	Cys	Cys	Cys	Ala	Cys	Cys	Cys	Cys	Cys	Thr	Gly	Ala	Ala			
	705					710					715				720			
Cys	Thr	Cys	Cys	Thr	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Cys	Cys	Gly	Thr			
				725						730					735			
Cys	Thr	Gly	Thr	Cys	Thr	Thr	Cys	Ala	Thr	Cys	Thr	Thr	Cys	Cys	Cys			
			740					745					750					
Cys	Cys	Cys	Ala	Ala	Ala	Ala	Cys	Cys	Cys	Ala	Ala	Gly	Gly	Ala	Cys			
	755						760					765						
Ala	Cys	Cys	Cys	Thr	Cys	Ala	Thr	Gly	Ala	Thr	Cys	Thr	Cys	Ala	Cys			
	770					775					780							
Gly	Cys	Ala	Cys	Cys	Cys	Cys	Cys	Gly	Ala	Gly	Gly	Thr	Cys	Ala	Cys			
	785				790					795					800			
Ala	Thr	Gly	Cys	Gly	Thr	Gly	Gly	Thr	Gly	Gly	Thr	Gly	Gly	Ala	Cys			
				805					810						815			
Gly	Thr	Gly	Ala	Gly	Cys	Cys	Ala	Gly	Gly	Ala	Thr	Gly	Ala	Cys	Cys			
			820					825					830					
Cys	Cys	Gly	Ala	Gly	Gly	Thr	Gly	Cys	Ala	Gly	Thr	Thr	Cys	Ala	Cys			
		835					840					845						
Ala	Thr	Gly	Gly	Thr	Ala	Cys	Ala	Thr	Ala	Ala	Ala	Cys	Ala	Ala	Cys			
	850					855				860								
Gly	Ala	Gly	Cys	Ala	Gly	Gly	Thr	Gly	Cys	Gly	Cys	Ala	Cys	Cys	Gly			
	865				870					875					880			
Cys	Cys	Cys	Gly	Gly	Cys	Cys	Gly	Cys	Cys	Gly	Cys	Thr	Ala	Cys	Gly			
				885						890					895			
Gly	Gly	Ala	Gly	Cys	Ala	Gly	Cys	Ala	Gly	Thr	Thr	Cys	Ala	Ala	Cys			
		900						905					910					
Ala	Gly	Cys	Ala	Cys	Gly	Ala	Thr	Cys	Cys	Gly	Cys	Gly	Thr	Gly	Gly			
	915						920					925						
Thr	Cys	Ala	Gly	Cys	Ala	Cys	Cys	Cys	Thr	Cys	Cys	Cys	Cys	Ala	Thr			
	930					935					940							
Cys	Gly	Cys	Gly	Cys	Ala	Cys	Cys	Ala	Gly	Gly	Ala	Cys	Thr	Gly	Gly			
	945				950					955					960			
Cys	Thr	Gly	Ala	Gly	Gly	Gly	Gly	Cys	Ala	Ala	Gly	Gly	Ala	Gly	Thr			
				965					970						975			
Thr	Cys	Ala	Ala	Gly	Thr	Gly	Cys	Ala	Ala	Ala	Gly	Thr	Cys	Cys	Ala			
		980						985					990					
Cys	Ala	Ala	Cys	Ala	Ala	Gly	Gly	Cys	Ala	Cys	Thr	Cys	Cys	Cys	Gly			
	995						1000					1005						
Gly	Cys	Cys	Cys	Cys	Cys	Ala	Thr	Cys	Gly	Ala	Gly	Ala	Ala	Ala	Ala			
	1010					1015					1020							
Cys	Cys	Ala	Thr	Cys	Thr	Cys	Cys	Ala	Ala	Ala	Gly	Cys	Cys	Ala	Gly			
	1025				1030					1035					1040			
Ala	Gly	Gly	Gly	Cys	Ala	Gly	Cys	Cys	Cys	Cys	Thr	Gly	Gly	Ala	Gly			
				1045						1050					1055			
Cys	Cys	Gly	Ala	Ala	Gly	Gly	Thr	Cys	Thr	Ala	Cys	Ala	Cys	Cys	Ala			
			1060					1065					1070					
Thr	Gly	Gly	Gly	Cys	Cys	Cys	Thr	Cys	Cys	Cys	Cys	Gly	Gly	Gly	Ala			
	1075						1080					1085						
Gly	Gly	Ala	Gly	Cys	Thr	Gly	Ala	Gly	Cys	Ala	Gly	Cys	Ala	Gly	Gly			
	1090					1095					1100							

Thr Cys Gly Gly Thr Cys Ala Gly Cys Cys Thr Gly Ala Cys Cys Thr
 1105 1110 1115 1120
 Gly Cys Ala Thr Gly Ala Thr Cys Ala Ala Cys Gly Gly Cys Thr Thr
 1125 1130 1135
 Cys Thr Ala Cys Cys Cys Thr Thr Cys Cys Gly Ala Cys Ala Thr Cys
 1140 1145 1150
 Thr Cys Gly Gly Thr Gly Gly Ala Gly Thr Gly Gly Gly Ala Gly Ala
 1155 1160 1165
 Ala Gly Ala Ala Cys Gly Gly Gly Ala Ala Gly Gly Cys Ala Gly Ala
 1170 1175 1180
 Gly Gly Ala Cys Ala Cys Thr Ala Cys Ala Ala Gly Ala Cys Cys
 1185 1190 1195 1200
 Ala Cys Gly Cys Cys Gly Gly Cys Cys Gly Thr Gly Cys Thr Gly Gly
 1205 1210 1215
 Ala Cys Ala Gly Cys Gly Ala Cys Gly Gly Cys Thr Cys Cys Thr Ala
 1220 1225 1230
 Cys Thr Thr Cys Cys Thr Cys Thr Ala Cys Ala Ala Cys Ala Ala Gly
 1235 1240 1245
 Cys Thr Cys Thr Cys Ala Gly Thr Gly Cys Cys Cys Ala Cys Gly Ala
 1250 1255 1260
 Gly Thr Gly Ala Gly Thr Gly Gly Cys Ala Gly Cys Gly Gly Gly Gly
 1265 1270 1275 1280
 Cys Gly Ala Cys Gly Thr Cys Thr Thr Cys Ala Cys Cys Thr Gly Cys
 1285 1290 1295
 Thr Cys Cys Gly Thr Gly Ala Thr Gly Cys Ala Cys Gly Ala Gly Gly
 1300 1305 1310
 Cys Cys Thr Thr Gly Cys Ala Cys Ala Ala Cys Cys Ala Cys Thr Ala
 1315 1320 1325
 Cys Ala Cys Gly Cys Ala Gly Ala Ala Gly Thr Cys Cys Ala Thr Cys
 1330 1335 1340
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 Ala Ala

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<400> 23
 Ser Tyr Asp Met Thr
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<210> 24
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 <212> PRT
 <213> Oryctolagus cuniculus

<400> 24
 Ser Tyr Asp Met Ser
 1 5

<210> 25
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 <212> PRT
 <213> Oryctolagus cuniculus

<400> 25
 Asp Tyr Asp Leu Ser
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<210> 26
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 <400> 26
 Ser Tyr Asp Met Ser
 1 5

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 <400> 27
 Tyr Ala Ser Gly Ser Thr Tyr Tyr
 1 5

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 <213> Oryctolagus cuniculus

 <400> 28
 Ser Ser Ser Gly Thr Thr Tyr Tyr
 1 5

 <210> 29
 <211> 8
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 <213> Oryctolagus cuniculus

 <400> 29
 Tyr Ala Ser Gly Ser Thr Tyr Tyr
 1 5

 <210> 30
 <211> 8
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 <213> Oryctolagus cuniculus

 <400> 30
 Ala Ile Asp Gly Asn Pro Tyr Tyr
 1 5

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 <212> PRT
 <213> Oryctolagus cuniculus

 <400> 31
 Ser Thr Ala Tyr Asn Ser His Tyr
 1 5

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 <213> Oryctolagus cuniculus

<400> 32
Glu His Ala Gly Tyr Ser Gly Asp Thr Gly His
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<210> 33
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<400> 33
Glu Gly Ala Gly Val Ser Met Thr
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Glu Asp Ala Gly Phe Ser Asn Ala
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<210> 35
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<400> 35
Gly Ala Gly Asp
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<213> Oryctolagus cuniculus

<400> 36
Gly Gly Ser Trp Leu Asp
1 5

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<213> Oryctolagus cuniculus

<400> 37
Arg Cys Ala Tyr Asp
1 5

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Arg Cys Ala Asp Val Val
1 5

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 Arg Cys Ala Leu Val
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 <400> 40
 Gln Ser Ile Ser Thr Tyr
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 <210> 41
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 <400> 41
 Gln Ser Val Ser Ser Tyr
 1 5

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 <213> Oryctolagus cuniculus

 <400> 42
 Glu Ser Ile Ser Asn Tyr
 1 5

 <210> 43
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 <213> Oryctolagus cuniculus

 <400> 43
 Lys Asn Val Tyr Asn Asn Asn Trp
 1 5

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 <213> Oryctolagus cuniculus

 <400> 44
 Gln Gln Gly Tyr Thr His Ser Asn Val Asp Asn Val
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 <210> 45
 <211> 12
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 45
 Gln Gln Gly Tyr Ser Ile Ser Asp Ile Asp Asn Ala
 1 5 10

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 <213> Oryctolagus cuniculus

 <400> 46
 Gln Cys Thr Ser Gly Gly Lys Phe Ile Ser Asp Gly Ala Ala
 1 5 10

 <210> 47
 <211> 11
 <212> PRT
 <213> Oryctolagus cuniculus

 <400> 47
 Ala Gly Asp Tyr Ser Ser Ser Ser Asp Asn Gly
 1 5 10

 <210> 48
 <211> 12
 <212> PRT
 <213> Oryctolagus cuniculus

 <400> 48
 Gln Ala Thr His Tyr Ser Ser Asp Trp Leu Thr Tyr
 1 5 10

 <210> 49
 <211> 5
 <212> RNA
 <213> Oryctolagus cuniculus

 <400> 49
 auuua 5

 <210> 50
 <211> 6
 <212> RNA
 <213> Oryctolagus cuniculus

 <400> 50
 auuuua 6

 <210> 51
 <211> 7
 <212> RNA
 <213> Oryctolagus cuniculus

 <400> 51
 auuuuua 7

 <210> 52
 <211> 157
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> A synthetic anti-CD83 heavy chain variable region sequence

<400> 52
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
20 25 30
Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser
35 40 45
Ser Tyr Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60
Trp Ile Gly Ile Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp
65 70 75 80
Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu
85 90 95
Glu Val Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ser
100 105 110
Arg Glu His Ala Gly Tyr Ser Gly Asp Thr Gly His Leu Trp Gly Pro
115 120 125
Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val
130 135 140
Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser
145 150 155

<210> 53
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic anti-CD83 heavy chain variable region
sequence

<400> 53
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Ser Pro
20 25 30
Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Leu Ser
35 40 45
Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60
Tyr Ile Gly Ile Ile Ser Ser Ser Gly Thr Thr Tyr Tyr Ala Asn Trp
65 70 75 80
Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu
85 90 95
Lys Val Thr Ser Pro Thr Ile Gly Asp Thr Ala Thr Tyr Phe Cys Ala
100 105 110
Arg Glu Gly Ala Gly Val Ser Met Thr Leu Trp Gly Pro Gly Thr Leu
115 120 125
Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu
130 135 140
Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser
145 150

<210> 54
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic anti-CD83 heavy chain variable region
sequence

<400> 54
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
20 25 30
Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser
35 40 45
Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60
Trp Ile Gly Ile Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp
65 70 75 80
Ala Lys Gly Arg Val Ala Ile Ser Lys Thr Ser Thr Thr Val Asp Leu
85 90 95
Lys Ile Thr Ser Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
100 105 110
Arg Glu Asp Ala Gly Phe Ser Asn Ala Leu Trp Gly Pro Gly Thr Leu
115 120 125
Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu
130 135 140
Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser
145 150

<210> 55
<211> 147
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic anti-CD83 light chain variable region
sequence

<400> 55
Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15
Leu Pro Gly Ala Arg Cys Ala Tyr Asp Met Thr Gln Thr Pro Ala Ser
20 25 30
Val Glu Val Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala Ser
35 40 45
Gln Ser Ile Ser Thr Tyr Leu Asp Trp Tyr Gln Gln Lys Pro Gly Gln
50 55 60
Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asp Leu Ala Ser Gly Val
65 70 75 80
Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr
85 90 95
Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
100 105 110
Gly Tyr Thr His Ser Asn Val Asp Asn Val Phe Gly Gly Gly Thr Glu
115 120 125
Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu Phe Pro
130 135 140
Pro Ser Ser
145

<210> 56
<211> 147
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic anti-CD83 light chain variable region
sequence

<400> 56
Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15
Leu Pro Gly Ala Arg Cys Ala Tyr Asp Met Thr Gln Thr Pro Ala Ser
20 25 30
Val Glu Val Ala Val Gly Gly Thr Val Ala Ile Lys Cys Gln Ala Ser
35 40 45
Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
50 55 60
Pro Pro Lys Pro Leu Ile Tyr Glu Ala Ser Met Leu Ala Ala Gly Val
65 70 75 80
Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95
Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
100 105 110
Gly Tyr Ser Ile Ser Asp Ile Asp Asn Ala Phe Gly Gly Gly Thr Glu
115 120 125
Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu Phe Pro
130 135 140
Pro Ser Ser
145

<210> 57
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic anti-CD83 light chain variable region
sequence

<400> 57
Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15
Leu Pro Gly Ala Arg Cys Ala Asp Val Val Met Thr Gln Thr Pro Ala
20 25 30
Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ala
35 40 45
Ser Glu Ser Ile Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
50 55 60
Gln Pro Pro Lys Leu Leu Ile Tyr Arg Thr Ser Thr Leu Ala Ser Gly
65 70 75 80
Val Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu
85 90 95
Thr Ile Ser Gly Val Gln Cys Asp Asp Val Ala Thr Tyr Tyr Cys Gln
100 105 110
Cys Thr Ser Gly Gly Lys Phe Ile Ser Asp Gly Ala Ala Phe Gly Gly
115 120 125
Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu
130 135 140
Leu Phe Pro Pro Ser Ser
145 150

<210> 58
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic M83 020B08L light chain sequence

<400> 58
Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15
Leu Pro Gly Ala Arg Cys Ala Tyr Asp Met Thr Gln Thr Pro Ala Ser
20 25 30
Val Glu Val Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala Ser
35 40 45
Gln Ser Ile Ser Thr Tyr Leu Asp Trp Tyr Gln Gln Lys Pro Gly Gln
50 55 60
Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asp Leu Ala Ser Gly Val
65 70 75 80
Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr
85 90 95
Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
100 105 110
Gly Tyr Thr His Ser Asn Val Asp Asn Val Phe Gly Gly Gly Thr Glu
115 120 125
Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu Phe Pro
130 135 140
Pro Ser Ser Asp Glu Val Ala Thr Gly Thr Val Thr Ile Val Cys Val
145 150 155 160
Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly
165 170 175
Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser
180 185 190
Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr
195 200 205
Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr
210 215 220
Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys
225 230 235

<210> 59
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic M83 020B08L anti-CD83 light chain sequence

<400> 59
atggacatga gggccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60
agatgtgcct atgatatgac ccagactcca gcctctgtgg aggtagctgt gggaggcaca 120
gtcaccatca agtgccaggc cagtcagagc attagtagct acttagactg gtatcagcag 180
aaaccagggc agcctcccaa gctcctgata tatgatgcat ccgatctggc atctgggggtc 240
ccatcgcggt tcaaaggcag tggatctggg acacagttca ctctcaccat cagcgacctg 300
gagtgtgccg atgctgccac ttactactgt caacagggtt atacacatag taatgttgat 360
aatgttttcg gcggagggac cgaggtgggt gtcaaagggt atccagttgc acctactgtc 420
ctcctcttcc caccatctag cgatgagggt gcaactggaa cagtcaccat cgtgtgtgtg 480
gcgaataaat actttcccga tgtcaccgtc acctgggagg tggatggcac caccctcaga 540
actggcatcg agaacagtaa aacaccgcag aattctgcag attgtaccta caacctcagc 600
agcactctga cactgaccag cacacagtac aacagccaca aagagtacac ctgcaagggtg 660
accaggggca cgacctcagt cgtccagagc ttcagtagga agaactgtta a 711

<210> 60
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic M83 020B08H heavy chain sequence

<400> 60

Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly
1				5					10					15	
Val	Gln	Cys	Gln	Ser	Val	Glu	Glu	Ser	Gly	Gly	Arg	Leu	Val	Thr	Pro
			20					25					30		
Gly	Thr	Pro	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Ser
		35					40					45			
Ser	Tyr	Asp	Met	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu
	50					55					60				
Trp	Ile	Gly	Ile	Ile	Tyr	Ala	Ser	Gly	Thr	Thr	Tyr	Tyr	Ala	Asn	Trp
65					70					75					80
Ala	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Thr	Ser	Thr	Thr	Val	Asp	Leu
				85					90					95	
Lys	Val	Thr	Ser	Pro	Thr	Ile	Gly	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	Ala
			100					105					110		
Arg	Glu	Gly	Ala	Gly	Val	Ser	Met	Thr	Leu	Trp	Gly	Pro	Gly	Thr	Leu
		115					120					125			
Val	Thr	Val	Ser	Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val	Phe	Pro	Leu
	130					135					140				
Ala	Pro	Cys	Cys	Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	Thr	Leu	Gly	Cys
145					150					155					160
Leu	Val	Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser
				165					170					175	
Gly	Thr	Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val	Arg	Gln	Ser
			180					185					190		
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr	Ser	Ser	Ser
	195					200						205			
Gln	Pro	Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn	Thr	Lys	Val
	210					215					220				
Asp	Lys	Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr	Cys	Pro	Pro
225					230					235					240
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro
				245					250					255	
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
			260					265					270		
Val	Asp	Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr	Trp	Tyr	Ile
	275						280					285			
Asn	Asn	Glu	Gln	Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg	Glu	Gln	Gln
	290					295					300				
Phe	Asn	Ser	Thr	Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile	Ala	His	Gln
305					310					315					320
Asp	Trp	Leu	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His	Asn	Lys	Ala
				325					330					335	
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Arg	Gly	Gln	Pro
			340					345					350		
Leu	Glu	Pro	Lys	Val	Tyr	Thr	Met	Gly	Pro	Pro	Arg	Glu	Glu	Leu	Ser
	355						360					365			
Ser	Arg	Ser	Val	Ser	Leu	Thr	Cys	Met	Ile	Asn	Gly	Phe	Tyr	Pro	Ser
	370					375					380				
Asp	Ile	Ser	Val	Glu	Trp	Glu	Lys	Asn	Gly	Lys	Ala	Glu	Asp	Asn	Tyr
385					390					395					400
Lys	Thr	Thr	Pro	Ala	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Leu	Tyr
				405					410					415	
Asn	Lys	Leu	Ser	Val	Pro	Thr	Ser	Glu	Trp	Gln	Arg	Gly	Asp	Val	Phe
			420					425					430		
Thr	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
		435					440					445			
Ser	Ile	Ser	Arg	Ser	Pro	Gly	Lys								
	450					455									

<210> 61
 <211> 1368
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A synthetic M83 020B08H anti-CD83 heavy chain
 sequence

<400> 61
 atggagacag gcttgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60
 tcggtggagg agtccggggg tcgcctgggc acgcctggga cacccttgac actcacctgc 120
 acagtctctg gattctccct cagcagctac gacatgacct gggtcgcgca ggctccaggg 180
 aaggggctgg aatggatcgg aatcatttat gctagtggta ccacatacta cgcgaactgg 240
 gcgaaaggcc gattcaccat ctccaaaacc tcgaccacgg tggatctgaa agtcaccagt 300
 ccgacaatcg gggacacggc cacctatttc tgtgccagag agggggctgg tgttagtatg 360
 accttgtggg gcccaggcac cctgggcacc gtctcctcag ggcaacctaa ggctccatca 420
 gtcttccccc tggcccccct ctgcggggac acaccctcta gcacggtgac cttggggtgc 480
 ctggtcaaag gctacctccc ggagccagtg accgtgacct ggaactcggg caccctcacc 540
 aatgggggtac gcaccttccc gtccgtccgg cagtccctcag gcctctactc gctgagcagc 600
 gtggtgagcg tgacctcaag cagccagccc gtcacctgca acgtggccca cccagccacc 660
 aacaccaaag tggacaagac cgttgcgccc tcgacatgca gcaagcccac gtgcccacc 720
 cctgaactcc tggggggacc gtctgtcttc atcttcccc caaaacccaa ggacaccctc 780
 atgatctcac gcacccccga ggtcacatgc gtggtggtgg acgtgagcca ggatgacccc 840
 gaggtgcagt tcacatggta cataaacaac gagcaggtgc gcaccgccc gcccgcgcta 900
 cgggagcagc agttcaacag cacgatccgc gtggtcagca cctccccat cgcgcaccag 960
 gactggctga ggggcaagga gttcaagtgc aaagtccaca acaaggcact cccggccccc 1020
 atcgagaaaa ccatctccaa agccagaggg cagcccctgg agccgaaggt ctacaccatg 1080
 ggccttcccc gggaggagct gagcagcagg tcggtcagcc tgacctgcat gatcaacggc 1140
 ttctaccctt ccgacatctc ggtggagtgg gagaagaacg ggaaggcaga ggacaactac 1200
 aagaccacgc cggcgtgct ggacagcgac ggctcctact tcctctacaa caagtctca 1260
 gtgcccacga gtgagtggca gcggggcgac gtcttcacct gctcgtgat gcacgaggcc 1320
 ttgcacaacc actacacgca gaagtccatc tcccgctctc cggtgaaa 1368

<210> 62
 <211> 236
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A synthetic M83 006G05L light chain sequence

<400> 62
 Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15
 Leu Pro Gly Ala Arg Cys Ala Tyr Asp Met Thr Gln Thr Pro Ala Ser
 20 25 30
 Val Glu Val Ala Val Gly Gly Thr Val Ala Ile Lys Cys Gln Ala Ser
 35 40 45
 Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 50 55 60
 Pro Pro Lys Pro Leu Ile Tyr Glu Ala Ser Met Leu Ala Ala Gly Val
 65 70 75 80
 Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 85 90 95
 Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 Gly Tyr Ser Ile Ser Asp Ile Asp Asn Ala Phe Gly Gly Gly Thr Glu
 115 120 125
 Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu Phe Pro
 130 135 140

```

Pro Ser Ser Asp Glu Val Ala Thr Gly Thr Val Thr Ile Val Cys Val
145          150          155          160
Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly
          165          170          175
Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser
          180          185          190
Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr
          195          200          205
Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr
          210          215          220
Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys
225          230          235

```

<210> 63
 <211> 711
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A synthetic M83 006G05L anti-CD83 light chain
 sequence

```

<400> 63
atggacatga gggccccac tcaactgctg gggctcctgc tgctctggct cccaggtgcc      60
agatgtgcct atgatatgac ccagactcca gcctctgtgg aggtagctgt gggaggcaca      120
gtcgccatca agtgccaggc cagtcagagc gttagtagtt acttagcctg gtatcagcag      180
aaaccagggc agcctcccaa gcccctgata tacgaagcat ccattgctggc ggctgggggc      240
tcacgcggtg tcaaaggcag tggatctggg acagacttca ctctcaccat cagcgacctg      300
gagtgtgacg atgctgccac ttactattgt caacagggtt attctatcag tgatattgat      360
aatgctttcg gcggaggggc cgagggtggtg gtcaaagggtg atccagttgc acctactgtc      420
ctcctcttcc caccatctag cgatgagggtg gcaactggaa cagtcaccat cgtgtgtgtg      480
gcgaataaat actttcccgga tgtcaccgtc acctggggagg tggatggcac caccctcagc      540
actggcatcg agaacagtaa aacaccgcag aattctgcag attgtacctt caacctcagc      600
agcactctga cactgaccag cacacagtac aacagccaca aagagtacac ctgcaagggtg      660
accaggggca cgacctcagt cgtccagagc ttcagtagga agaactgtta a              711

```

<210> 64
 <211> 459
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A synthetic M83 006G05L heavy chain sequence

```

<400> 64
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
 1          5          10          15
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Ser Pro
          20          25          30
Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Leu Ser
          35          40          45
Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
          50          55          60
Tyr Ile Gly Ile Ile Ser Ser Ser Gly Ser Thr Tyr Tyr Ala Ser Trp
65          70          75          80
Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu
          85          90          95
Glu Val Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ser
          100          105          110
Arg Glu His Ala Gly Tyr Ser Gly Asp Thr Gly His Leu Trp Gly Pro
          115          120          125

```

Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val
130						135					140				
Phe	Pro	Leu	Ala	Pro	Cys	Cys	Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	Thr
145					150					155					160
Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr
				165					170					175	
Trp	Asn	Ser	Gly	Thr	Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val
			180					185					190		
Arg	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr
		195					200					205			
Ser	Ser	Ser	Gln	Pro	Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn
		210				215					220				
Thr	Lys	Val	Asp	Lys	Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr
225					230					235					240
Cys	Pro	Pro	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro
				245					250					255	
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
			260					265					270		
Cys	Val	Val	Val	Asp	Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr
		275					280					285			
Trp	Tyr	Ile	Asn	Asn	Glu	Gln	Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg
	290					295					300				
Glu	Gln	Gln	Phe	Asn	Ser	Thr	Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile
305					310					315					320
Ala	His	Gln	Asp	Trp	Leu	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His
			325						330					335	
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Arg
		340						345					350		
Gly	Gln	Pro	Leu	Glu	Pro	Lys	Val	Tyr	Thr	Met	Gly	Pro	Pro	Arg	Glu
		355					360					365			
Glu	Leu	Ser	Ser	Arg	Ser	Val	Ser	Leu	Thr	Cys	Met	Ile	Asn	Gly	Phe
	370					375					380				
Tyr	Pro	Ser	Asp	Ile	Ser	Val	Glu	Trp	Glu	Lys	Asn	Gly	Lys	Ala	Glu
385					390					395					400
Asp	Asn	Tyr	Lys	Thr	Thr	Pro	Ala	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr
			405						410					415	
Phe	Leu	Tyr	Asn	Lys	Leu	Ser	Val	Pro	Thr	Ser	Glu	Trp	Gln	Arg	Gly
			420						425				430		
Asp	Val	Phe	Thr	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
	435						440					445			
Thr	Gln	Lys	Ser	Ile	Ser	Arg	Ser	Pro	Gly	Lys					
450						455									

<210> 65

<211> 1377

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic M83 006G05L anti-CD83 heavy chain sequence

<400> 65

atggagacag	gcctgcgctg	gcttctcctg	gtcgctgtgc	tcaaaggtgt	ccagtgtcag	60
tcgggtggagg	agtcgggggg	tcgcctgggc	tcgcctggga	caccctgac	actcacctgc	120
acagcctctg	gattctccct	cagtagctac	gacatgagct	gggtccgcca	ggctccaggg	180
aaggggctgg	aatacatcgg	aatcattagt	agtagtggtg	gcacatacta	cgcgagctgg	240
gcgaaaggcc	gattcaccat	ctccaaaacc	tcgaccacgg	tggatctgga	agtgaccagt	300
ctgacaaccg	aggacacggc	cacctatttc	tgtagtagag	aacatgctgg	ttatagtggg	360
gatacgggtc	acttgtgggg	cccaggcacc	ctgggtcaccg	tctcctcgga	gcaacctaag	420

```

gctccatcag tcttcccact ggccccctgc tgcggggaca caccctctag caccgtgacc 480
ttgggctgcc tgggtcaaagg ctacctcccg gagccagtga ccgtgacctg gaactcgggc 540
accctcacca atgggggtacg caccctcccg tccgtccggc agtcctcagg cctctactcg 600
ctgagcagcg tgggtgagcgt gacctcaagc agccagcccg tcacctgcaa cgtggcccac 660
ccagccacca acaccaaagt ggacaagacc gttgcgcctt cgacatgcag caagcccacg 720
tgcccccccc ctgaactcct ggggggaccg tctgtcttca tcttcccccc aaaacccaag 780
gacacctca tgatctcacg ccccccgag gtcacatgcg tgggtggtgga cgtgagccag 840
gatgaccccg aggtgcagtt cacatggtac ataaacaacg agcaggtgcg caccgcccgg 900
ccgccgctac gggagcagca gttcaacagc acgatccgcg tggtcagcac cctccccatc 960
gcgccaccag actgggtgag gggcaaggag ttcaagtgc aagtccacaa caaggcactc 1020
ccggccccca tcgagaaaac catctccaaa gccagagggc agcccctgga gccgaaggtc 1080
tacaccatgg gccctccccg ggaggagctg agcagcaggt cggtcagcct gacctgcatg 1140
atcaacggct tctacccttc cgacatctcg gtggagtggg agaagaacgg gaaggcagag 1200
gacaactaca agaccacgcc ggccgtgctg gacagcgacg gctcctactt cctctacaac 1260
aagctctcag tgcccacgag tgagtggcag cggggcgacg tcttcacctg ctccgtgatg 1320
cacgaggcct tgcacaacca ctacacgcag aagtccatct cccgctctcc gggtaaaa 1377

```

<210> 66

<211> 150

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic anti-CD83 heavy chain variable region
sequence

<400> 66

```

Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1      5      10      15
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
20      25      30
Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser
35      40      45
Asp Tyr Asp Leu Ser Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Lys
50      55      60
Tyr Ile Gly Phe Ile Ala Ile Asp Gly Asn Pro Tyr Tyr Ala Thr Trp
65      70      75      80
Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu
85      90      95
Lys Ile Thr Ala Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
100     105     110
Arg Gly Ala Gly Asp Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser
115     120     125
Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro Cys Cys
130     135     140
Gly Asp Thr Pro Ser Ser
145     150

```

<210> 67

<211> 152

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic anti-CD83 heavy chain variable region
sequence

<400> 67

```

Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1      5      10      15
Val His Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
20      25      30

```

Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Arg Ser
 35 40 45
 Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 50 55 60
 Trp Val Gly Val Ile Ser Thr Ala Tyr Asn Ser His Tyr Ala Ser Trp
 65 70 75 80
 Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu
 85 90 95
 Lys Met Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
 100 105 110
 Arg Gly Gly Ser Trp Leu Asp Leu Trp Gly Gln Gly Thr Leu Val Thr
 115 120 125
 Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro
 130 135 140
 Cys Cys Gly Asp Thr Pro Ser Ser
 145 150

<210> 68
 <211> 149
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A synthetic anti-CD83 light chain variable region
 sequence

<400> 68
 Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15
 Leu Pro Gly Ala Arg Cys Ala Asp Val Val Met Thr Gln Thr Pro Ala
 20 25 30
 Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser
 35 40 45
 Ser Lys Asn Val Tyr Asn Asn Asn Trp Leu Ser Trp Phe Gln Gln Lys
 50 55 60
 Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala
 65 70 75 80
 Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly Ser Gly Thr Gln Phe
 85 90 95
 Thr Leu Thr Ile Ser Asp Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr
 100 105 110
 Cys Ala Gly Asp Tyr Ser Ser Ser Ser Asp Asn Gly Phe Gly Gly Gly
 115 120 125
 Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu
 130 135 140
 Phe Pro Pro Ser Ser
 145

<210> 69
 <211> 149
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> SITE
 <222> (1)...(149)
 <223> Xaa = any amino acid

<220>
 <223> A synthetic anti-CD83 light chain variable region
 sequence

<400> 69
Met Asp Xaa Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15
Leu Pro Gly Ala Arg Cys Ala Leu Val Met Thr Gln Thr Pro Ala Ser
20 25 30
Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser Ser
35 40 45
Gln Ser Val Tyr Asp Asn Asp Glu Leu Ser Trp Tyr Gln Gln Lys Pro
50 55 60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Lys Leu Ala Ser
65 70 75 80
Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Ala
85 90 95
Leu Thr Ile Ser Gly Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys
100 105 110
Gln Ala Thr His Tyr Ser Ser Asp Trp Tyr Leu Thr Phe Gly Gly Gly
115 120 125
Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu
130 135 140
Phe Pro Pro Ser Ser
145

<210> 70
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic 96G08 light chain sequence

<400> 70
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15
Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Ala Ser Pro
20 25 30
Val Ser Ala Pro Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser Ser
35 40 45
Gln Ser Val Tyr Asn Asn Asp Phe Leu Ser Trp Tyr Gln Gln Lys Pro
50 55 60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala Ser
65 70 75 80
Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr
85 90 95
Leu Thr Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys
100 105 110
Thr Gly Thr Tyr Gly Asn Ser Ala Trp Tyr Glu Asp Ala Phe Gly Gly
115 120 125
Gly Thr Glu Val Val Val Lys Arg Thr Pro Val Ala Pro Thr Val Leu
130 135 140
Leu Phe Pro Pro Ser Ser Ala Glu Leu Ala Thr Gly Thr Ala Thr Ile
145 150 155 160
Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Gly Thr Val Thr Trp Lys
165 170 175
Val Asp Gly Ile Thr Gln Ser Ser Gly Ile Asn Asn Ser Arg Thr Pro
180 185 190
Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
195 200 205
Ser Ser Asp Glu Tyr Asn Ser His Asp Glu Tyr Thr Cys Gln Val Ala
210 215 220
Gln Asp Ser Gly Ser Pro Val Val Gln Ser Phe Ser Arg Lys Ser Cys
225 230 235 240

<210> 71
 <211> 13
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 71
 Gln Ser Ser Gln Ser Val Tyr Asn Asn Asp Phe Leu Ser
 1 5 10

<210> 72
 <211> 7
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 72
 Tyr Ala Ser Thr Leu Ala Ser
 1 5

<210> 73
 <211> 13
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 73
 Thr Gly Thr Tyr Gly Asn Ser Ala Trp Tyr Glu Asp Ala
 1 5 10

<210> 74
 <211> 723
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A synthetic 96G08 anti-CD83 light chain sequence

<400> 74
 atggacacga gggccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60
 acatttgcg aagtgctgac ccagactgca tcgcccgtgt ctgcacctgt gggaggcaca 120
 gtcaccatca attgccagtc cagtcagagt gtttataata acgacttctt atcctgggat 180
 cagcagaaac cagggcagcc tcccaaactc ctgatctatt atgcatccac tctggcatct 240
 ggggtcccat cccggttcaa aggcagtgga tctgggacac agttcactct caccatcagc 300
 gacctggagt gtgacgatgc tgccacttac tactgtacag gcacttatgg taatagtgtc 360
 tggtagcagg atgctttcgg cggagggacc gaggtggtgg tcaaactgtac gccagttgca 420
 cctactgtcc tcctcttccc accatctagc gctgagctgg caactggaac agccaccatc 480
 gtgtgcgtgg cgaataaata ctttcccgat ggcaccgtca cctggaaggt ggatggcatc 540
 acccaaagca gcggcatcaa taacagtaga acaccgcaga attctgcaga ttgtacctac 600
 aacctcagca gtactctgac actgagcagc gacgagtaca acagccacga cgagtacacc 660
 tgccaggtgg cccaggactc aggctcaccg gtcgtccaga gcttcagtag gaagagctgt 720
 tag 723

<210> 75
 <211> 25
 <212> DNA
 <213> Oryctolagus cuniculus

<400> 75
 cagtccagtc agagtgttta taata 25

<210> 76
 <211> 20
 <212> DNA
 <213> Oryctolagus cuniculus

<400> 76
 atgcatccac tctggcatct

20

<210> 77
 <211> 25
 <212> DNA
 <213> Oryctolagus cuniculus

<400> 77
 acaggcactt atggtaatag tgctt

25

<210> 78
 <211> 456
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A synthetic 96G08 heavy chain sequence

<400> 78
 Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
 1 5 10 15
 Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
 20 25 30
 Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser
 35 40 45
 Ser Asp Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 50 55 60
 Trp Ile Gly Ile Ile Ser Ser Gly Gly Asn Thr Tyr Tyr Ala Ser Trp
 65 70 75 80
 Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu
 85 90 95
 Lys Met Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
 100 105 110
 Arg Val Val Gly Gly Thr Tyr Ser Ile Trp Gly Gln Gly Thr Leu Val
 115 120 125
 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Tyr Pro Leu Ala
 130 135 140
 Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu
 145 150 155 160
 Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly
 165 170 175
 Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp
 180 185 190
 Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro
 195 200 205
 Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys
 210 215 220
 Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile
 225 230 235 240
 Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro
 245 250 255
 Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val
 260 265 270
 Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val
 275 280 285

Asp	Asp	Val	Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Pro	Arg	Glu	Glu	Gln
290						295					300				
Phe	Asn	Ser	Thr	Phe	Arg	Ser	Val	Ser	Glu	Leu	Pro	Ile	Met	His	Gln
305					310					315					320
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Phe	Lys	Cys	Arg	Val	Asn	Ser	Ala	Ala
			325						330					335	
Phe	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Arg	Pro
		340					345						350		
Lys	Ala	Pro	Gln	Val	Tyr	Thr	Ile	Pro	Pro	Pro	Lys	Glu	Gln	Met	Ala
	355					360						365			
Lys	Asp	Lys	Val	Ser	Leu	Thr	Cys	Met	Ile	Thr	Asp	Phe	Phe	Pro	Glu
	370					375					380				
Asp	Ile	Thr	Val	Glu	Trp	Gln	Trp	Asn	Gly	Gln	Pro	Ala	Glu	Asn	Tyr
385					390					395					400
Lys	Asn	Thr	Gln	Pro	Ile	Met	Asp	Thr	Asp	Gly	Ser	Tyr	Phe	Val	Tyr
			405						410					415	
Ser	Lys	Leu	Asn	Val	Gln	Lys	Ser	Asn	Trp	Glu	Ala	Gly	Asn	Thr	Phe
			420					425					430		
Thr	Cys	Ser	Val	Leu	His	Glu	Gly	Leu	His	Asn	His	His	Thr	Glu	Lys
	435						440					445			
Ser	Leu	Ser	His	Ser	Pro	Gly	Lys								
	450					455									

<210> 79
 <211> 5
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 79
 Ser Asp Gly Ile Ser
 1 5

<210> 80
 <211> 16
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 80
 Ile Ile Ser Ser Gly Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
 1 5 10 15

<210> 81
 <211> 8
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 81
 Val Val Gly Gly Thr Tyr Ser Ile
 1 5

<210> 82
 <211> 1371
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A synthetic 96G08 anti-CD83 heavy chain sequence

<400> 82
 atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaagggtg ccagtgtcag 60
 tcggtggagg agtccggggg tcgcctgggc acacctggga caccctgac actcacctgc 120

Ser Gln Ser Val Tyr Gly Asn Asn Glu Leu Ser Trp Tyr Gln Gln Lys
 50 55 60
 Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gln Ala Ser Ser Leu Ala
 65 70 75 80
 Ser Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe
 85 90 95
 Thr Leu Thr Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr
 100 105 110
 Cys Leu Gly Glu Tyr Ser Ile Ser Ala Asp Asn His Phe Gly Gly Gly
 115 120 125
 Thr Glu Val Val Val Lys Arg Thr Pro Val Ala Pro Thr Val Leu Leu
 130 135 140
 Phe Pro Pro Ser Ser Ala Glu Leu Ala Thr Gly Thr Ala Thr Ile Val
 145 150 155 160
 Cys Val Ala Asn Lys Tyr Phe Pro Asp Gly Thr Val Thr Trp Lys Val
 165 170 175
 Asp Gly Ile Thr Gln Ser Ser Gly Ile Asn Asn Ser Arg Thr Pro Gln
 180 185 190
 Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Ser
 195 200 205
 Ser Asp Glu Tyr Asn Ser His Asp Glu Tyr Thr Cys Gln Val Ala Gln
 210 215 220
 Asp Ser Gly Ser Pro Val Val Gln Ser Phe Ser Arg Lys Ser Cys
 225 230 235

<210> 87
 <211> 13
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 87
 Gln Ser Ser Gln Ser Val Tyr Gly Asn Asn Glu Leu Ser
 1 5 10

<210> 88
 <211> 7
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 88
 Gln Ala Ser Ser Leu Ala Ser
 1 5

<210> 89
 <211> 11
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 89
 Leu Gly Glu Tyr Ser Ile Ser Ala Asp Asn His
 1 5 10

<210> 90
 <211> 720
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A synthetic 95F04 anti-CD83 light chain sequence

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<400> 90
atggacacga gggccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc      60
acatttgccc aagccgtggt gaccagact acatcgcccg tgtctgcacc tgtgggaggc      120
acagtcacca tcaattgcca gtccagtcag agtggttatg gtaacaacga attatcctgg      180
tatcagcaga aaccagggca gcctcccaag ctctgatct accaggcatc cagcctggca      240
tctgggggtcc catcgcggtt caaaggcagt ggatctggga cacagttcac tctcaccatc      300
agcgacctgg agtgtgacga tgctgccact tactactgtc taggcgaata tagcattagt      360
gctgataatc atttcggcgg agggaccgag gtgggtgtca aacgtacgcc agttgcacct      420
actgtcctcc tcttcccacc atctagcgct gagctggcaa ctggaacagc caccatcgtg      480
tgcgtggcga ataaatactt tcccgatggc accgtcacct ggaaggtgga tggcatcacc      540
caaagcagcg gcatcaataa cagtagaaca ccgcagaatt ctgcagattg tacctacaac      600
ctcagcagta ctctgacact gagcagcgac gagtacaaca gccacgacga gtacacctgc      660
caggtggccc aggactcagg ctcaccggtc gtccagagct tcagtaggaa gagctgttag      720

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<210> 91

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic 95F04 heavy chain sequence

<400> 91

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Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
 1           5           10           15
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
          20           25           30
Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser
          35           40           45
Ser Asn Ala Met Ile Trp Val Arg Gln Ala Pro Arg Glu Gly Leu Glu
          50           55           60
Trp Ile Gly Ala Met Asp Ser Asn Ser Arg Thr Tyr Tyr Ala Thr Trp
65           70           75           80
Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Ser Ile Thr Val Asp
          85           90           95
Leu Lys Ile Thr Ser Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys
          100          105          110
Ala Arg Gly Asp Gly Gly Ser Ser Asp Tyr Thr Glu Met Trp Gly Pro
          115          120          125
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
          130          135          140
Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
145          150          155          160
Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
          165          170          175
Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
          180          185          190
Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
          195          200          205
Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala
          210          215          220
Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys
225          230          235          240
Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe
          245          250          255
Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
          260          265          270
Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe
          275          280          285
Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro
290          295          300

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Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro
 305 310 315 320
 Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val
 325 330 335
 Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
 340 345 350
 Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys
 355 360 365
 Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp
 370 375 380
 Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro
 385 390 395 400
 Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser
 405 410 415
 Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala
 420 425 430
 Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His
 435 440 445
 His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 450 455 460

<210> 92
 <211> 5
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 92
 Ser Asn Ala Met Ile
 1 5

<210> 93
 <211> 16
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 93
 Ala Met Asp Ser Asn Ser Arg Thr Tyr Tyr Ala Thr Trp Ala Lys Gly
 1 5 10 15

<210> 94
 <211> 11
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 94
 Gly Asp Gly Gly Ser Ser Asp Tyr Thr Glu Met
 1 5 10

<210> 95
 <211> 1383
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A synthetic 95F04 anti-CD83 heavy chain sequence

<400> 95
 atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaagggtg ccagtgtcag 60
 tcggtggagg agtccggggg tcgcctgggc acgcctggga caccctgac actcacctgc 120
 acagtctctg gaatcgacct cagtagcaat gcaatgatct ggggccgcca ggctccaagg 180
 gaggggctgg aatggatcgg agccatggat agtaatagta ggacgtacta cgcgacctgg 240
 gcgaaaggcc gattcaccat ctccagaacc tcgtcgatta cgggtgatct gaaaatcacc 300

agtccgacaa	ccgaggacac	ggccacctat	ttctgtgcc	gaggggatgg	tggcagtagt	360
gattatacag	agatgtgggg	cccagggacc	ctcgtcaccg	tctcgagcgc	ttctacaaag	420
ggcccatctg	tctatccact	ggcccttgga	tctgctgccc	aaactaactc	catggtgacc	480
ctgggatgcc	tgggtcaaggg	ctatttccct	gagccagtga	cagtgaacctg	gaactctgga	540
tccctgtcca	gcggtgtgca	caccttccca	gctgtcctgc	agtctgacct	ctacactctg	600
agcagctcag	tgactgtccc	ctccagcacc	tggcccagcg	agaccgtcac	ctgcaacggt	660
gcccaccccg	ccagcagcac	caaggtggac	aagaaaattg	tgccagggga	ttgtggttgt	720
aagccttgca	tatgtacagt	cccagaagta	tcattctgtct	tcattcttccc	cccaaagccc	780
aaggatgtgc	tcaccattac	tctgactcct	aaggtcacgt	gtgttggtgt	agacatcagc	840
aaggatgatc	ccgaggtcca	gttcagctgg	tttgtagatg	atgtggaggt	gcacacagct	900
cagacgcaac	cccgggagga	gcagttcaac	agcactttcc	gctcagtcag	tgaacttccc	960
atcatgcacc	aggactggct	caatggcaag	gagttcaa	gcaggtcaa	cagtgcagct	1020
ttccctgccc	ccatcgagaa	aaccatctcc	aaaaccaaag	gcagaccgaa	ggctccacag	1080
gtgtacacca	ttccacctcc	caaggagcag	atggccaagg	ataaagtcag	tctgacctgc	1140
atgataacag	acttcttccc	tgaagacatt	actgtggagt	ggcagtgga	tgggcagcca	1200
gcggaagact	acaagaacac	tcagcccatc	atggacacag	atggctctta	cttcgtctac	1260
agcaagctca	atgtgcagaa	gagcaactgg	gaggcaggaa	atactttcac	ctgctctgtg	1320
ttacatgagg	gcctgcacaa	ccaccatact	gagaagagcc	tctcccactc	tcctggtaaa	1380
tga						1383

<210> 96

<211> 1383

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic 95F04 anti-CD83 light chain sequence

<400> 96

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tcggtggagg	agtccggggg	tcgcctggtc	acgcctggga	caccctgac	actcacctgc	120
acagtctctg	gaatcgacct	cagtagcaat	gcaatgatct	gggtccgcca	ggctccaagg	180
gaggggctgg	aatggatcgg	agccatggat	agtaatagta	ggacgtacta	cgcgacctgg	240
gcgaaaggcc	gattcaccat	ctccagaacc	tcgtcgatta	cggtggatct	gaaaatcacc	300
agtccgacaa	ccgaggacac	ggccacctat	ttctgtgcc	gaggggatgg	tggcagtagt	360
gattatacag	agatgtgggg	cccagggacc	ctcgtcaccg	tctcgagcgc	ttctacaaag	420
ggcccatctg	tctatccact	ggcccttgga	tctgctgccc	aaactaactc	catggtgacc	480
ctgggatgcc	tgggtcaaggg	ctatttccct	gagccagtga	cagtgaacctg	gaactctgga	540
tccctgtcca	gcggtgtgca	caccttccca	gctgtcctgc	agtctgacct	ctacactctg	600
agcagctcag	tgactgtccc	ctccagcacc	tggcccagcg	agaccgtcac	ctgcaacggt	660
gcccaccccg	ccagcagcac	caaggtggac	aagaaaattg	tgccagggga	ttgtggttgt	720
aagccttgca	tatgtacagt	cccagaagta	tcattctgtct	tcattcttccc	cccaaagccc	780
aaggatgtgc	tcaccattac	tctgactcct	aaggtcacgt	gtgttggtgt	agacatcagc	840
aaggatgatc	ccgaggtcca	gttcagctgg	tttgtagatg	atgtggaggt	gcacacagct	900
cagacgcaac	cccgggagga	gcagttcaac	agcactttcc	gctcagtcag	tgaacttccc	960
atcatgcacc	aggactggct	caatggcaag	gagttcaa	gcaggtcaa	cagtgcagct	1020
ttccctgccc	ccatcgagaa	aaccatctcc	aaaaccaaag	gcagaccgaa	ggctccacag	1080
gtgtacacca	ttccacctcc	caaggagcag	atggccaagg	ataaagtcag	tctgacctgc	1140
atgataacag	acttcttccc	tgaagacatt	actgtggagt	ggcagtgga	tgggcagcca	1200
gcggaagact	acaagaacac	tcagcccatc	atggacacag	atggctctta	cttcgtctac	1260
agcaagctca	atgtgcagaa	gagcaactgg	gaggcaggaa	atactttcac	ctgctctgtg	1320
ttacatgagg	gcctgcacaa	ccaccatact	gagaagagcc	tctcccactc	tcctggtaaa	1380
tga						1383

<210> 97

<211> 107

<212> PRT

<213> Homo sapiens

<400> 97

Pro	Glu	Val	Lys	Val	Ala	Cys	Ser	Glu	Asp	Val	Asp	Leu	Pro	Cys	Thr
1				5					10					15	

Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu
20 25 30
Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu
35 40 45
Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala
50 55 60
Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys
65 70 75 80
Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg
85 90 95
Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr
100 105

<210> 98
<211> 8
<212> PRT
<213> Oryctolagus cuniculus

<400> 98
Gln Ser Val Tyr Asp Asn Asp Glu
1 5

<210> 99
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic 96G08 anti-CD83 light chain sequence

<400> 99
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acatttgcg aagtgctgac ccagactgca tcgcccgtgt ctgcacctgt gggaggcaca 120
gtcaccatca attgccagtc cagtcagagt gtttataata acgacttctt atcctgggat 180
cagcagaaac cagggcagcc tcccaaactc ctgatctatt atgcatccac tctggcatct 240
ggggtcccat cccggttcaa aggcagtgga tctgggacac agttcactct caccatcagc 300
gacctggagt gtgacgatgc gccacttact actgtacagg cacttatggg aatagtgttt 360
ggtacgagga tgctttcggc ggagggaccg aggtgggtgt caaacgtacg ccagttgcac 420
ctactgtcct cctcttccca ccatctagcg ctgagctggc aactggaaca gccaccatcg 480
tgtgcgtggc gaataaatac tttcccgatg gcaccgtcac ctggaagggt gatggcatca 540
cccaaagcag cggcatcaat aacagtagaa caccgcagaa ttctgcagat tgtacctaca 600
acctcagcag tactctgaca ctgagcagcg acgagtacaa cagccacgac gactacacct 660
gccaggtggc ccaggactca ggctcaccgg tcgtccagag cttcagtagg aagagctgtt 720